



RECEIVED

MAY 21 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Tamatani, Takuya
Tezuka, Katsunari

<120> CELL SURFACE MOLECULE MEDIATING CELL
ADHESION AND SIGNAL TRANSMISSION

<130> 06501-039001

<140> US 09/383,551

<141> 1999-08-26

<150> PCT/JP98/00837

<151> 1998-02-27

<150> JAPAN 09-62290

<151> 1997-02-27

<150> JAPAN 10-62217

<151> 1998-02-26

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(597)

<400> 1

atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa 48
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata 96
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc 144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat 192
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta 288
 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95

tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca 336
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110

att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg 384
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125

cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc 432
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt 480
 Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
 145 150 155 160

att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct 528
 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
 165 170 175

aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct 576
 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
 180 185 190

aga ctc aca gat gtg acc cta taa 600
 Arg Leu Thr Asp Val Thr Leu
 195

<210> 2
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1 5 10 15
 Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
 20 25 30
 Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
 35 40 45
 Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
 65 70 75 80
 Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
 115 120 125
 His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
 130 135 140

C. canis

3

Ile	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Cys	Ile	Leu	Gly	Cys	Ile	Leu
145					150					155					160
Ile	Cys	Trp	Leu	Thr	Lys	Lys	Lys	Tyr	Ser	Ser	Ser	Val	His	Asp	Pro
				165					170					175	
Asn	Gly	Glu	Tyr	Met	Phe	Met	Arg	Ala	Val	Asn	Thr	Ala	Lys	Lys	Ser
			180					185					190		
Arg	Leu	Thr	Asp	Val	Thr	Leu									
			195												

<210> 3
 <211> 2610
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (26)...(622)

<400> 3

ggactgttaa	ctgtttctgg	caaac	atg	aag	tca	ggc	ctc	tgg	tat	ttc	ttt					52
			Met	Lys	Ser	Gly	Leu	Trp	Tyr	Phe	Phe					
			1				5									
ctc	ttc	tgc	ttg	cgc	att	aaa	gtt	tta	aca	gga	gaa	atc	aat	ggt	tct	100
Leu	Phe	Cys	Leu	Arg	Ile	Lys	Val	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	
10				15					20						25	
gcc	aat	tat	gag	atg	ttt	ata	ttt	cac	aac	gga	ggt	gta	caa	att	tta	148
Ala	Asn	Tyr	Glu	Met	Phe	Ile	Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Leu	
				30				35						40		
tgc	aaa	tat	cct	gac	att	gtc	cag	caa	ttt	aaa	atg	cag	ttg	ctg	aaa	196
Cys	Lys	Tyr	Pro	Asp	Ile	Val	Gln	Gln	Phe	Lys	Met	Gln	Leu	Leu	Lys	
			45				50						55			
ggg	ggg	caa	ata	ctc	tgc	gat	ctc	act	aag	aca	aaa	gga	agt	gga	aac	244
Gly	Gly	Gln	Ile	Leu	Cys	Asp	Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	
		60				65						70				
aca	gtg	tcc	att	aag	agt	ctg	aaa	ttc	tgc	cat	tct	cag	tta	tcc	aac	292
Thr	Val	Ser	Ile	Lys	Ser	Leu	Lys	Phe	Cys	His	Ser	Gln	Leu	Ser	Asn	
	75					80				85						
aac	agt	gtc	tct	ttt	ttt	cta	tac	aac	ttg	gac	cat	tct	cat	gcc	aac	340
Asn	Ser	Val	Ser	Phe	Phe	Leu	Tyr	Asn	Leu	Asp	His	Ser	His	Ala	Asn	
90					95				100					105		
tat	tac	ttc	tgc	aac	cta	tca	att	ttt	gat	cct	cct	cct	ttt	aaa	gta	388
Tyr	Tyr	Phe	Cys	Asn	Leu	Ser	Ile	Phe	Asp	Pro	Pro	Pro	Phe	Lys	Val	
				110					115					120		
act	ctt	aca	gga	gga	tat	ttg	cat	att	tat	gaa	tca	caa	ctt	tgt	tgc	436
Thr	Leu	Thr	Gly	Gly	Tyr	Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	
			125					130					135			
cag	ctg	aag	ttc	tgg	tta	ccc	ata	gga	tgt	gca	gcc	ttt	gtt	gta	gtc	484
Gln	Leu	Lys	Phe	Trp	Leu	Pro	Ile	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	

C1
Cons

140	145	150	
tgc att ttg gga tgc ata ctt att tgt tgg ctt	aca aaa aag aag tat	532	
Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu	Thr Lys Lys Lys Tyr		
155	160	165	
tca tcc agt gtg cac gac cct aac ggt gaa tac	atg ttc atg aga gca	580	
Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr	Met Phe Met Arg Ala		
170	175	180	185
gtg aac aca gcc aaa aaa tct aga ctc aca gat	gtg acc cta	622	
Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp	Val Thr Leu		
190	195		
taatatggaa ctctggcacc caggcatgaa gcacgttggc	cagttttcct caacttgaag	682	
tgcaagattc tcttatttcc gggaccacgg agagtctgac	ttaactacat acatcttctg	742	
ctgggtgtttt gttcaatctg gaagaatgac tgtatcagtc	aatggggatt ttaacagact	802	
gccttggtac tgccgagtc tctcaaaaca aacacctct	tgcaaccagc tttggagaaa	862	
gccagctcc tgtgtgtctca ctgggagtgg aatccctgtc	tccacatctg ctcctagcag	922	
tgcatcagcc agtaaaacaa acacatttac aagaaaaatg	ttttaaagat gccaggggta	982	
ctgaatctgc aaagcaaag agcagccaag gaccagcatc	tgtccgcatt tcactatcat	1042	
actacctctt ctttctgtag ggrtgagaat tcctcttcta	atcagtcaag ggagatgctt	1102	
caaagctggr gctattttat ttctgagatg ttgatgtgaa	ctgtacatta gtacatactc	1162	
agtactctcc ttcaattgct gaaccccgat tgaccatttt	accaagactt tagatgcttt	1222	
cttgtgccct caattttctt tttaaaaata cttctacatg	actgcttgac agcccaacag	1282	
ccactctcaa tagagagcta tgtcttacat tctttcctct	gctgctcaat agttttatat	1342	
atctatgcat acatatatac acacatatgt atataaaatt	cataatgaat atatttgcct	1402	
atattctccc tacaagaata tttttgctcc agaaagacat	gttcttttct caaattcagt	1462	
taaaatgggt tactttgttc aagtttagtg taggaaacat	tgcccggaat tgaaagcaaa	1522	
tttawwtat tatcctattt tctaccatta tctatgtttt	catggtgcta ttaattacaa	1582	
gtttagtctt tttttagat catattaaaa ttgcaaaaca	aatcatcttt aatgggccag	1642	
cattctcatg gggtagagca gaatattcat ttagcctgaa	agctgcagtt actatagggt	1702	
gctgtcagac tatacccatg gtgcctctgg gcttgacagg	tcaaaatgggt ccccatcagc	1762	
ctggagcagc cctccagacc tgggtggaat tccagggttg	agagactccc ctgagccaga	1822	
ggccactagg tattcttget cccagaggct gaagtcaccc	tgggaatcac agtgggtctac	1882	
ctgcattcat aattccagga tctgtgaaga gcacatatgt	gtcagggcac aattccctct	1942	
cataaaaacc acacagcctg gaaattggcc ctggcccttc	aagatagcct tctttagaat	2002	
atgatttggc tagaaagatt cttaaatatg tggaatatga	ttattcttag ctggaatatt	2062	
ttctctactt cctgtctgca tgcccaaggc ttctgaagca	gccaatgtcg atgcaacaac	2122	
atttgtaaact ttaggtaaac tgggattatg ttgtagttta	acattttgta actgtgtgct	2182	
tatagtttac aagtgtgagc cgatatgtca ttatgcatac	ttatattatc ttaagcatgt	2242	
gtaatgctgg atgtgtacag tacagtacwt aacttgtaat	ttgaatctag tatgggtgttc	2302	
tgttttcagc tgacttggtg aacctgactg gctttgcaca	ggtgttccct gagttgtttg	2362	
caggtttctg tgtgtgggtt ggggtatggg gaggagaacc	ttcatggtgg cccacctggc	2422	
ctggttgtcc aagctgtgcc tcgacacatc ctcatcccaa	gcatgggaca cctcaagatg	2482	
aataataatt cacaaaattt ctgtgaaatc aaatccagtt	ttaagaggag ccacttatca	2542	
aagagatttt aacagtagta agaaggcaaa gaataaacat	ttgatattca gcaactgaaa	2602	
aaaaaaaa		2610	

<210> 4

<211> 2072

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (35)...(634)

C1
cons

tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct 684
Ser
200

```

gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac 744
tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa 804
tttcagcaga ctgccctggg tttgctgagt ccttttaagg caaacccctt cttatagaag 864
acccggtca tatgtattca acaaacagac ctcaactggga tacaatcccc tctttctgcg 924
cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa 984
tgccagggtg tgaatctgta aagtacacag gcagccattg accaccgtct gtcctcgttt 1044
tttcagattc tatttttttc catagagatc agcattcctt ctagaatcag acagtagagg 1104
gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt 1164
accaccatgt tctctaaca cttctatat ccagctgac actgcttcag ggcttagatg 1224
cctgcttttg ccttcaagtc tccccttaaa gatactccca caggtctact tgggtggcctg 1284
cagccactct gaataggaag tttggtctac aatttccccc ctctgctgct caaaaaaaaa 1344
aattagtaga tatgattttt ccatattctc aatgccaaag taattttttt cagcaaaagac 1404
atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa cattttctcag 1464
aatcaaaagc aaattaattt tgcggtggtg tttttctacc attatcttgg gtttccatgg 1524
tgctattact cacaagttta gctatttttt tatgcatcat attaaagttg caagcaagca 1584
gagcaaccct cggttaatgg gcaaacattc tcctggggta gaatgaattg tctatttagc 1644
ccgaaaactg cagtttctgt ggggtggctgc cagactacag ccgtgctttg ctctggcttt 1704
gacaggttga aatagycccc atgascstgg aacagwactc cagactgtgc tggagtccca 1764
aagttaggag ggccatggag cctgggacag gctgctgctt tggcttttag gatctaggaa 1824
raattacaga ggggccaaga cagagttccc tcccctagaa actgtgcagc ctggaagtca 1884
gccctggcac ttttaagatag ccttcttttag aacatgagtt agttggtagt attctgacgt 1944
gtaaacagcc tatkgttgct cggagctgga ccattttctc cacttccctg tctgcatgcc 2004
taagacttct agagcagcca acgtatatgc aacattaaag aaaaaaaaaa aaaaaaaaaa 2064
aaaaaaaaa 2072

```

<210> 5
 <211> 603
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(600)

<400> 5
 atg aag ccg tac ttc tgc cat gtc ttt gtc ttc tgc ttc cta atc aga 48
 Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
 1 5 10 15
 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca 96
 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 20 25 30
 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 35 40 45
 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 50 55 60
 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
 65 70 75 80
 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288

*C1
coris*

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

ccc gta ggg ttg cca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480
Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145 150 155 160

ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
165 170 175

cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190

tct aga ctt gca ggt gtg acc tca taa 603
Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 6
<211> 836
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (35)...(682)

<400> 6
ctggaggggga agagtgcagc tggttcctggc agac atg aag ccc tac ttc tcg tgc 55
Met Lys Pro Tyr Phe Ser Cys
1 5

gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
10 15 20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
25 30 35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
40 45 50 55

C1
Covis

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
 60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
 75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
 90 95 100

ggc agc tac ttt tta tgc agc ctg tgc att ttc gac cca ccc cct ttt 391
 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
 105 110 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439
 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
 120 125 130 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487
 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
 140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
 155 160 165

Cis
cons
 aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583
 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
 170 175 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca 631
 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala
 185 190 195

ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg 679
 Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg
 200 205 210 215

aat taatttggtt atttctattt taaaagaaag acattttttc ccctaaagat 732
 Asn

aatttttgta tttttatgtg aaagtctgaa tcttcatttt aactcgactt atatactctg 792
 tggatatatta aaaataatgt ttgtgaaaaa aaaaaaaaaa aaaa 836

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 7

ctgctcgaga tgaagcccta cttctcg

27

<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 8

accctacggg taacggatcc ttcagctggc aa

32

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 9

taactgtttc tcgagaacat gaagtcaggc

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 10

atcctatggg taacggatcc ttcagctggc

30

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 11

cgtgatattg ctgaagagct tggcggcgaa tgggc

35

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 12

cattcaagtt tcagggaact agtccatgcg tttc

34

C1
Cen's

<210> 13
 <211> 200
 <212> PRT
 <213> Rattus norvegicus

<400> 13

Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1 5 10 15
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
 20 25 30
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
 145 150 155 160
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
 165 170 175
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
 180 185 190
 Ser Arg Leu Ala Gly Met Thr Ser
 195 200

<210> 14
 <211> 200
 <212> PRT
 <213> Mus musculus

<400> 14

Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
 1 5 10 15
 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
 20 25 30
 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140

C
 Conus

Pro	Val	Gly	Leu	Pro	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile
145					150					155					160
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp
				165					170					175	
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys
			180					185					190		
Ser	Arg	Leu	Ala	Gly	Val	Thr	Ser								
		195					200								

<210> 15
 <211> 216
 <212> PRT
 <213> Rattus norvegicus

<400> 15

Met	Lys	Pro	Tyr	Phe	Ser	Cys	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys
1				5				10						15	
Leu	Leu	Thr	Gly	Glu	Leu	Asn	Asp	Leu	Ala	Asn	His	Arg	Met	Phe	Ser
			20					25					30		
Phe	His	Asp	Gly	Gly	Val	Gln	Ile	Ser	Cys	Asn	Tyr	Pro	Glu	Thr	Val
		35					40					45			
Gln	Gln	Leu	Lys	Met	Gln	Leu	Phe	Lys	Asp	Arg	Glu	Val	Leu	Cys	Asp
	50					55					60				
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Thr	Val	Ser	Ile	Lys	Asn	Pro
65					70					75				80	
Met	Ser	Cys	Pro	Tyr	Gln	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85					90					95	
Asp	Asn	Ala	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Phe	Leu	Cys	Ser	Leu	Ser
			100					105					110		
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Lys	Asn	Leu	Ser	Gly	Gly	Tyr
		115					120					125			
Leu	Leu	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu
	130					135					140				
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Ala	Ala	Leu	Leu	Phe	Gly	Cys	Ile
145					150					155					160
Phe	Ile	Val	Trp	Phe	Ala	Lys	Lys	Lys	Tyr	Arg	Ser	Ser	Val	His	Asp
				165					170					175	
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys
			180					185					190		
Ser	Arg	Leu	Ala	Gly	Thr	Ala	Pro	Leu	Arg	Ala	Leu	Gly	Arg	Gly	Glu
		195					200					205			
His	Ser	Ser	Cys	Gln	Asp	Arg	Asn								
		210				215									

<210> 16
 <211> 200
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(200)
 <223> Xaa = Any Amino Acid

<400> 16

Met	Lys	Pro	Tyr	Phe	Xaa	Xaa	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys
1				5					10					15	
Leu	Leu	Thr	Gly	Glu	Xaa	Asn	Xaa	Xaa	Ala	Asn	His	Arg	Met	Phe	Ser
			20					25					30		
Phe	His	Xaa	Gly	Gly	Val	Gln	Ile	Ser	Cys	Xaa	Tyr	Pro	Glu	Thr	Val
		35				40					45				
Gln	Gln	Leu	Lys	Met	Gln	Leu	Phe	Lys	Xaa	Arg	Glu	Val	Leu	Cys	Asp
	50					55				60					
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Thr	Val	Ser	Ile	Lys	Asn	Pro
65					70				75					80	
Met	Xaa	Cys	Xaa	Tyr	Gln	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85				90						95	
Xaa	Asn	Xaa	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Xaa	Xaa	Cys	Ser	Leu	Ser
			100					105					110		
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Xaa	Asn	Leu	Ser	Gly	Gly	Tyr
		115					120					125			
Leu	Xaa	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu
	130					135					140				
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Xaa	Xaa	Leu	Leu	Phe	Gly	Cys	Ile
145					150					155					160
Xaa	Ile	Xaa	Trp	Phe	Xaa	Lys	Lys	Lys	Tyr	Xaa	Ser	Ser	Val	His	Asp
				165				170						175	
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys
			180					185					190		
Ser	Arg	Leu	Ala	Gly	Xaa	Thr	Xaa								
		195					200								

<210> 17
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(214)
 <223> Xaa = Any Amino Acid

<400> 17

Met	Leu	Xaa	Leu	Xaa	Leu	Ala	Trp	Xaa	Leu	Xaa	Leu	Phe	Xaa	Leu	Xaa
1				5					10					15	
Ile	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Val	Xaa	Gln	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Ala	Xaa	Xaa	Asn	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Lys	Tyr	Xaa	Xaa
		35				40					45				
Pro	Xaa	Xaa	Xaa	Xaa	Glu	Phe	Arg	Xaa	Xaa	Leu	Leu	Lys	Gly	Xaa	Asp
	50					55				60					
Ser	Xaa	Val	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Thr	Tyr	Xaa	Xaa	Gly	Asn
65					70				75					80	
Xaa	Val	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Gly	Xaa	Leu	Ser	Asn
				85				90					95		
Asn	Ser	Val	Xaa	Phe	Xaa	Leu	Gln	Asn	Leu	Xaa	Xaa	Xaa	Xaa	Thr	Xaa
			100					105					110		
Xaa	Tyr	Phe	Cys	Lys	Xaa	Glu	Xaa	Met	Tyr	Pro	Pro	Pro	Tyr	Xaa	Xaa
		115				120						125			
Xaa	Xaa	Xaa	Asn	Gly	Thr	Xaa	Ile	His	Val	Xaa	Xaa	Xaa	Xaa	Leu	Cys

130		135		140
Pro Xaa Xaa Xaa Phe Xaa Xaa Trp Xaa Leu Xaa Xaa Val Xaa Xaa Xaa				
145		150		155
Leu Xaa Xaa Tyr Ser Xaa Leu Xaa Thr Ala Xaa Ile Xaa Xaa Xaa Xaa				160
		165		170
Xaa Lys Lys Arg Ser Xaa Leu Xaa Xaa Gly Xaa Tyr Met Xaa Met Xaa				175
		180		185
Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa Gln Pro Tyr Xaa Xaa				190
		195		200
Asp Phe Xaa Xaa Xaa Xaa				205
210				

<210> 18
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Tyr Pro Pro Pro Tyr
 1 5

<210> 19
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 19
 Tyr Met Asn Met
 1

<210> 20
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 20
 Tyr Val Lys Met
 1

<210> 21
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 21
 Phe Asp Pro Pro Pro Phe
 1 5

<210> 22
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 22
 Tyr Met Phe Met
 1

Cs
Cons

<210> 23
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> (1)...(216)
 <223> Xaa = Any Amino Acid

<400> 23
 Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1 5 10 15
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
 20 25 30
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
 35 40 45
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
 50 55 60
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
 65 70 75 80
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
 85 90 95
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
 100 105 110
 Ile Phe Asp Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
 115 120 125
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
 130 135 140
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
 145 150 155 160
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
 165 170 175
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
 180 185 190
 Ser Arg Leu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215

<210> 24
 <211> 16
 <212> PRT
 <213> Rattus norvegicus

<400> 24
 Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg Asn
 1 5 10 15

<210> 25
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 25

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
 1 5 10 15
 Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
 20 25 30
 Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
 35 40 45
 Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
 50 55 60
 Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
 65 70 75 80
 Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
 85 90 95
 Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
 100 105 110
 Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125
 Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140
 Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
 145 150 155 160
 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175
 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190
 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
 195 200 205
 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
 210 215 220

<210> 26
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
 1 5 10 15
 Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
 20 25 30
 Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
 35 40 45
 Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
 50 55 60
 Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
 65 70 75 80
 Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
 85 90 95
 Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
 100 105 110
 Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
 115 120 125
 Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly
 130 135 140
 Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
 145 150 155 160
 Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
 165 170 175

C1
cons

C1
cont

Tyr	Ser	Phe	Leu	Leu	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys
			180					185					190		
Arg	Ser	Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu
		195					200					205			
Pro	Glu	Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn	
	210					215					220				
